STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 162536

TO:	From:
Vanessa L Ford **Location: rem/3B25/3C18** **Art Unit: 1645** **Tuesday, August 16, 2005** **Case Serial Number: 09/884465**	**Mary Jane Ruhl** **Location: Biotech-Chem Library** **Remsen 1-A-62** **Phone: 571-272-2524** **maryjane.ruhl@uspto.gov**

Search Notes

Examiner Ford,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

162588

MP

From: Chan, Christina
Sent: Monday, August 15, 2005 6:57 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: in re: 09/884465 sequence search

Please rush. Thanks Chris

Chris Chan
SPE, 1644
TC 1600 New Hire Training Coordinator
571-272-0841
Remsen 3E89

-----Original Message-----
From: Ford, Vanessa
Sent: Monday, August 15, 2005 6:42 PM
To: Chan, Christina
Subject: in re: 09/884465 sequence search

Please search SEQ ID NO:332. Please include interference searches. Please rush. Please provide at least 60 hits.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
art unit:1645

STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:21 ; Search time 26 Seconds
(without alignments)
2601.233 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MQITYTDDEIQVAKLAGKYT.....IELRLPSGEVIKKNLSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3375	71.4	1039	4	US-09-583-110-5226	Sequence 5226, Ap
2	3280	69.4	708	4	US-09-107-433-4231	Sequence 4231, Ap
3	1314.5	27.8	678	4	US-09-107-433-4992	Sequence 4992, Ap
4	1314.5	27.8	838	4	US-09-583-110-5225	Sequence 5225, Ap
5	1302.5	27.5	838	4	US-09-468-656A-4	Sequence 4, Appli
6	946	20.0	830	4	US-09-107-433-4309	Sequence 4309, Ap
7	946	20.0	851	4	US-09-583-110-3850	Sequence 3850, Ap
8	937.5	19.8	819	4	US-09-468-656A-10	Sequence 10, Appl
9	818.5	17.3	763	3	US-08-961-083-66	Sequence 66, Appl
10	818.5	17.3	763	4	US-09-536-784-66	Sequence 66, Appl
11	637	13.5	819	4	US-09-468-656A-8	Sequence 8, Appli
12	636	13.5	796	3	US-08-961-083-56	Sequence 56, Appl
13	636	13.5	796	4	US-09-536-784-56	Sequence 56, Appl
14	636	13.5	816	4	US-09-645-835A-7	Sequence 7, Appli
15	635	13.4	321	4	US-09-107-433-2993	Sequence 2993, Ap
16	631	13.3	829	4	US-09-583-110-3851	Sequence 3851, Ap
17	470	9.9	484	4	US-09-468-656A-6	Sequence 6, Appli
18	431	9.1	447	3	US-08-961-083-182	Sequence 182, App
19	431	9.1	447	4	US-09-536-784-182	Sequence 182, App
20	230	4.9	825	4	US-09-645-835A-2	Sequence 2, Appli
21	223.5	4.7	822	4	US-09-645-835A-6	Sequence 6, Appli
22	223.5	4.7	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
23	217.5	4.6	5024	4	US-09-710-279-2964	Sequence 2964, Ap
24	199.5	4.2	1098	3	US-08-923-992A-8	Sequence 8, Appli
25	195.5	4.1	1128	3	US-08-923-992A-6	Sequence 6, Appli
26	194.5	4.1	1164	3	US-08-923-992A-2	Sequence 2, Appli
27	192	4.1	571	3	US-08-961-083-4	Sequence 4, Appli
28	192	4.1	571	4	US-09-536-784-4	Sequence 4, Appli
29	192	4.1	1164	3	US-08-923-992A-10	Sequence 10, Appl
30	191.5	4.1	3696	3	US-09-134-001C-5080	Sequence 5080, Ap
31	190	4.0	1596	4	US-08-978-277A-4	Sequence 4, Appli
32	187	4.0	1155	4	US-09-710-279-1780	Sequence 1780, Ap
33	185.5	3.9	1104	3	US-08-923-992A-4	Sequence 4, Appli
34	185	3.9	1742	4	US-09-386-962C-4	Sequence 4, Appli
35	185	3.9	1742	4	US-09-386-959-4	Sequence 4, Appli
36	184.5	3.9	1964	2	US-08-790-912-3	Sequence 3, Appli
37	184.5	3.9	2052	2	US-08-790-912-2	Sequence 2, Appli
38	184	3.9	8991	4	US-08-714-741-32	Sequence 32, Appl
39	182	3.8	984	1	US-08-242-932-2	Sequence 2, Appli
40	182	3.8	984	1	US-08-714-481-2	Sequence 2, Appli
41	182	3.8	984	5	PCT-US95-06111-2	Sequence 2, Appli
42	180.5	3.8	1183	2	US-08-447-031A-2	Sequence 2, Appli
43	178	3.8	2753	4	US-09-949-016-7659	Sequence 7659, Ap
44	178	3.8	2753	4	US-09-949-016-7660	Sequence 7660, Ap
45	175.5	3.7	952	4	US-09-107-532A-4706	Sequence 4706, Ap
46	175.5	3.7	1231	3	US-08-904-263A-4	Sequence 4, Appli
47	175.5	3.7	1231	4	US-09-434-123A-4	Sequence 4, Appli
48	175	3.7	1183	3	US-09-134-001C-3530	Sequence 3530, Ap
49	174	3.7	3924	4	US-09-538-092-1246	Sequence 1246, Ap
50	172.5	3.6	1965	4	US-09-583-110-3829	Sequence 3829, Ap
51	172.5	3.6	1972	4	US-09-107-433-3251	Sequence 3251, Ap
52	172	3.6	1279	4	US-09-710-279-3188	Sequence 3188, Ap
53	171	3.6	917	4	US-09-248-796A-18960	Sequence 18960, A
54	171	3.6	1240	4	US-09-538-092-658	Sequence 658, App
55	170.5	3.6	1545	3	US-08-296-791-4	Sequence 4, Appli
56	170.5	3.6	1545	4	US-09-839-996-4	Sequence 4, Appli
57	170.5	3.6	1545	4	US-10-080-505-4	Sequence 4, Appli
58	170.5	3.6	1545	4	US-10-645-655-4	Sequence 4, Appli
59	170.5	3.6	1545	5	PCT-US95-10661A-4	Sequence 4, Appli
60	170	3.6	1848	3	US-08-296-791-6	Sequence 6, Appli
61	170	3.6	1848	4	US-09-839-996-6	Sequence 6, Appli
62	170	3.6	1848	4	US-10-080-505-6	Sequence 6, Appli
63	170	3.6	1848	4	US-10-645-655-6	Sequence 6, Appli
64	170	3.6	1848	5	PCT-US95-10661A-6	Sequence 6, Appli
65	169.5	3.6	1306	4	US-09-134-000C-6670	Sequence 6670, Ap
66	169	3.6	639	4	US-09-823-240A-5	Sequence 5, Appli
67	168.5	3.6	171	4	US-09-107-433-3778	Sequence 3778, Ap
68	168.5	3.6	1315	4	US-09-200-650E-5	Sequence 5, Appli
69	168.5	3.6	3135	1	US-08-323-170B-2	Sequence 2, Appli
70	168.5	3.6	3135	3	US-08-954-441-2	Sequence 2, Appli
71	167.5	3.5	1226	4	US-09-248-796A-19043	Sequence 19043, A
72	167	3.5	783	6	5231168-2	Patent No. 5231168
73	167	3.5	783	6	5231168-2	Patent No. 5231168
74	166.5	3.5	160	4	US-09-583-110-5230	Sequence 5230, Ap
75	166.5	3.5	905	4	US-09-248-796A-16333	Sequence 16333, A
76	165.5	3.5	1181	3	US-09-206-898-23	Sequence 23, Appl
77	165	3.5	1437	4	US-09-949-016-10535	Sequence 10535, A
78	164.5	3.5	962	4	US-09-071-035-246	Sequence 246, App
79	164.5	3.5	962	4	US-09-071-035-250	Sequence 250, App
80	164.5	3.5	962	4	US-09-071-035-254	Sequence 254, App
81	164.5	3.5	962	4	US-09-071-035-470	Sequence 470, App
82	164.5	3.5	962	4	US-09-071-035-474	Sequence 474, App
83	164.5	3.5	962	4	US-09-071-035-478	Sequence 478, App
84	164	3.5	1164	2	US-08-589-756-1	Sequence 1, Appli
85	164	3.5	1164	3	US-09-206-800-1	Sequence 1, Appli
86	164	3.5	1164	3	US-09-206-898-1	Sequence 1, Appli
87	163.5	3.5	910	4	US-09-270-767-42083	Sequence 42083, A
88	163.5	3.5	1881	3	US-09-233-086-3	Sequence 3, Appli
89	163	3.4	890	4	US-09-583-110-5012	Sequence 5012, Ap
90	162.5	3.4	1781	4	US-09-961-403-13	Sequence 13, Appl
91	162	3.4	2123	3	US-08-968-685A-10	Sequence 10, Appl
92	161	3.4	676	3	US-09-134-001C-4318	Sequence 4318, Ap
93	161	3.4	825	4	US-09-248-796A-16538	Sequence 16538, A
94	161	3.4	1167	2	US-08-589-756-2	Sequence 2, Appli
95	161	3.4	1167	3	US-09-206-800-2	Sequence 2, Appli
96	161	3.4	1167	3	US-09-206-898-2	Sequence 2, Appli
97	160.5	3.4	1301	4	US-09-071-035-234	Sequence 234, App
98	160.5	3.4	1301	4	US-09-071-035-238	Sequence 238, App
99	160.5	3.4	1301	4	US-09-071-035-242	Sequence 242, App
100	160.5	3.4	1323	4	US-09-248-796A-19543	Sequence 19543, A

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:20 ; Search time 86 Seconds
(without alignments)
4074.476 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MQITYTDDEIQVAKLAGKYT.....IELRLPSGEVIKKNLSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : A_Geneseq_16Dec04:*
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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4728	100.0	907	5	AAU84065	Aau84065 S. pneumo
2	4723	99.9	907	5	AAU84061	Aau84061 S. pneumo
3	4705	99.5	907	5	AAU84063	Aau84063 S. pneumo
4	4702.5	99.5	908	7	ABM18896	Abm18896 S. pneumo
5	4693.5	99.3	908	7	ABM18897	Abm18897 S. pneumo
6	4675	98.9	901	5	AAU84067	Aau84067 S. pneumo
7	4675	98.9	906	7	ABM18795	Abm18795 S. pneumo
8	4675	98.9	906	8	ADP18483	Adp18483 S pneumon
9	4672	98.8	901	5	AAU84068	Aau84068 S. pneumo
10	4668.5	98.7	908	7	ABM18903	Abm18903 S. pneumo
11	4663	98.6	901	5	AAU84074	Aau84074 S. pneumo
12	4663	98.6	901	5	AAU84072	Aau84072 S. pneumo
13	4661	98.6	918	7	ABM18925	Abm18925 S. pneumo
14	4659.5	98.6	902	7	ABM18879	Abm18879 S. pneumo
15	4659.5	98.6	907	7	ABM18893	Abm18893 S. pneumo
16	4659.5	98.6	908	7	ABM18902	Abm18902 S. pneumo
17	4656.5	98.5	902	5	AAU84076	Aau84076 S. pneumo
18	4655.5	98.5	917	7	ABM18926	Abm18926 S. pneumo
19	4654.5	98.4	907	7	ABM18894	Abm18894 S. pneumo
20	4654	98.4	932	7	ABM18923	Abm18923 S. pneumo
21	4653.5	98.4	929	7	ABM18921	Abm18921 S. pneumo
22	4653.5	98.4	931	7	ABM18924	Abm18924 S. pneumo
23	4652.5	98.4	902	5	AAU84078	Aau84078 S. pneumo
24	4650.5	98.4	901	7	ABM18892	Abm18892 S. pneumo
25	4649.5	98.3	925	7	ABM18922	Abm18922 S. pneumo
26	4649.5	98.3	929	7	ABM18920	Abm18920 S. pneumo
27	4634	98.0	938	7	ABM18927	Abm18927 S. pneumo
28	4624	97.8	895	5	AAU84069	Aau84069 S. pneumo
29	4619	97.7	895	5	AAU84070	Aau84070 S. pneumo
30	4616.5	97.6	901	7	ABM18891	Abm18891 S. pneumo
31	4615	97.6	895	5	AAU84073	Aau84073 S. pneumo
32	4615	97.6	895	5	AAU84075	Aau84075 S. pneumo
33	4608.5	97.5	896	5	AAU84077	Aau84077 S. pneumo
34	4608.5	97.5	896	5	AAU84080	Aau84080 S. pneumo
35	4604.5	97.4	896	5	AAU84079	Aau84079 S. pneumo
36	4571	96.7	889	5	AAU84071	Aau84071 S. pneumo
37	4560.5	96.5	890	5	AAU84081	Aau84081 S. pneumo
38	4518	95.6	1152	5	AAU84054	Aau84054 S. pneumo
39	4518	95.6	1152	7	ABM18838	Abm18838 S. pneumo
40	4518	95.6	1378	5	AAU84053	Aau84053 S. pneumo
41	4518	95.6	1378	7	ABM18837	Abm18837 S. pneumo
42	4307	91.1	842	7	ABM18895	Abm18895 S. pneumo
43	4229.5	89.5	913	5	AAU84059	Aau84059 S. pneumo
44	4229.5	89.5	913	7	ABM18843	Abm18843 S. pneumo
45	4229.5	89.5	1139	5	AAU84055	Aau84055 S. pneumo
46	4229.5	89.5	1139	7	ABM18839	Abm18839 S. pneumo
47	4147	87.7	1365	5	AAU84057	Aau84057 S. pneumo
48	4147	87.7	1365	7	ABM18841	Abm18841 S. pneumo
49	4014.5	84.9	1238	5	AAU84056	Aau84056 S. pneumo
50	4014.5	84.9	1238	7	ABM18840	Abm18840 S. pneumo
51	3848.5	81.4	1126	5	AAU84058	Aau84058 S. pneumo
52	3848.5	81.4	1126	7	ABM18842	Abm18842 S. pneumo
53	3596	76.1	999	5	AAU84051	Aau84051 S. pneumo
54	3596	76.1	999	7	ABM18835	Abm18835 S. pneumo
55	3375	71.4	1019	3	AAB12722	Aab12722 Streptoco
56	3375	71.4	1019	3	AAB12751	Aab12751 Streptoco
57	3375	71.4	1019	5	AAU84021	Aau84021 Trunvated
58	3375	71.4	1019	7	ABM18802	Abm18802 S. pneumo
59	3375	71.4	1039	3	AAB12715	Aab12715 Streptoco
60	3375	71.4	1039	5	AAU75932	Aau75932 Streptoco
61	3375	71.4	1039	7	ABM18796	Abm18796 S. pneumo
62	3375	71.4	1039	8	ADK48711	Adk48711 Streptoco
63	3359	71.0	1019	3	AAB12753	Aab12753 Streptoco
64	3359	71.0	1019	3	AAB12752	Aab12752 Streptoco
65	3359	71.0	1019	3	AAB12748	Aab12748 Streptoco
66	3357	71.0	1019	3	AAB12750	Aab12750 Streptoco
67	3357	71.0	1039	6	ABU01419	Abu01419 S. pneumo
68	3356	71.0	1019	3	AAB12749	Aab12749 Streptoco
69	3300.5	69.8	807	5	AAU83997	Aau83997 Truncated
70	3300.5	69.8	807	7	ABM18833	Abm18833 S. pneumo
71	3298	69.8	632	5	AAU84009	Aau84009 Truncated
72	3298	69.8	633	7	ABM18800	Abm18800 S. pneumo
73	3298	69.8	633	7	ABM18854	Abm18854 S. pneumo
74	3298	69.8	901	5	AAU84066	Aau84066 S. pneumo
75	3298	69.8	907	5	AAU84060	Aau84060 S. pneumo
76	3298	69.8	907	5	AAU84064	Aau84064 S. pneumo
77	3293	69.6	632	5	AAU84006	Aau84006 Truncated
78	3293	69.6	632	5	AAU84013	Aau84013 Truncated
79	3293	69.6	633	7	ABM18856	Abm18856 S. pneumo
80	3293	69.6	633	7	ABM18851	Abm18851 S. pneumo
81	3293	69.6	633	7	ABM18855	Abm18855 S. pneumo
82	3293	69.6	633	7	ABM18858	Abm18858 S. pneumo
83	3293	69.6	902	7	ABM18878	Abm18878 S. pneumo
84	3293	69.6	908	7	ABM18901	Abm18901 S. pneumo
85	3293	69.6	908	7	ABM18899	Abm18899 S. pneumo
86	3293	69.6	908	7	ABM18898	Abm18898 S. pneumo
87	3293	69.6	908	7	ABM18900	Abm18900 S. pneumo
88	3288	69.5	632	5	AAU83998	Aau83998 Truncated
89	3288	69.5	644	5	AAU83996	Aau83996 Truncated
90	3288	69.5	644	7	ABM18829	Abm18829 S. pneumo
91	3284	69.5	632	5	AAU84003	Aau84003 Truncated
92	3284	69.5	632	5	AAU84004	Aau84004 Truncated
93	3284	69.5	632	5	AAU84012	Aau84012 Truncated
94	3284	69.5	633	7	ABM18857	Abm18857 S. pneumo
95	3284	69.5	633	7	ABM18848	Abm18848 S. pneumo
96	3284	69.5	633	7	ABM18849	Abm18849 S. pneumo
97	3283	69.4	632	5	AAU84015	Aau84015 Truncated
98	3283	69.4	633	7	ABM18852	Abm18852 S. pneumo

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:20 ; Search time 180 Seconds
(without alignments)
2577.465 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MQITYTDDEIQVAKLAGKYT.....IELRLPSGEVIKKNLSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3359	71.0	1019	2	Q6WNQ5	Q6wnq5 streptococc
2	3357	71.0	1039	2	Q9ANY1	Q9any1 streptococc
3	3356	71.0	1039	2	Q6WNQ7	Q6wnq7 streptococc
4	3356	71.0	1039	2	Q8DQ07	Q8dq07 streptococc
5	1307.5	27.7	819	2	Q6WNP9	Q6wnp9 streptococc
6	1307.5	27.7	839	2	Q9ANY2	Q9any2 streptococc
7	1300.5	27.5	816	2	Q6WNP6	Q6wnp6 streptococc
8	1300.5	27.5	830	2	Q6WNP5	Q6wnp5 streptococc
9	1273.5	26.9	811	2	Q6WNQ0	Q6wnq0 streptococc
10	1273.5	26.9	825	2	Q6WNQ1	Q6wnq1 streptococc
11	1249	26.4	834	2	Q6WNP8	Q6wnp8 streptococc
12	1245	26.3	853	2	Q8DQ08	Q8dq08 streptococc
13	946.5	20.0	819	2	Q97QM9	Q97qm9 streptococc
14	946	20.0	807	2	Q6T304	Q6t304 streptococc
15	946	20.0	811	2	Q6WNQ3	Q6wnq3 streptococc
16	946	20.0	844	2	Q9AG74	Q9ag74 streptococc
17	946	20.0	855	2	Q8CWR4	Q8cwr4 streptococc
18	935.5	19.8	819	2	Q9ANY3	Q9any3 streptococc
19	636	13.5	802	2	Q97QM8	Q97qm8 streptococc
20	636	13.5	816	2	Q9AHT9	Q9aht9 streptococc
21	636	13.5	817	2	Q6T8D7	Q6t8d7 streptococc
22	636	13.5	828	2	Q8DPQ2	Q8dpq2 streptococc
23	233	4.9	825	2	Q93GT5	Q93gt5 streptococc
24	230	4.9	825	2	Q99XV4	Q99xv4 streptococc
25	227	4.8	794	2	Q877Y2	Q877y2 streptococc
26	227	4.8	823	2	Q8K5Q1	Q8k5q1 streptococc
27	226.5	4.8	822	2	Q8E4U1	Q8e4u1 streptococc
28	225	4.8	823	2	Q8NZ82	Q8nz82 streptococc
29	223.5	4.7	822	2	Q9ZHG7	Q9zhg7 streptococc
30	223.5	4.7	9439	2	Q8CP76	Q8cp76 staphylococ
31	222.5	4.7	822	2	Q8DZ81	Q8dz81 streptococc
32	222.5	4.7	9196	2	Q8IQ87	Q8iq87 drosophila
33	220.5	4.7	861	2	Q6VVE5	Q6vve5 plasmodium
34	220	4.7	2762	2	Q9VGW4	Q9vgw4 drosophila
35	217.5	4.6	1800	2	Q8IEI9	Q8iei9 plasmodium
36	217	4.6	2651	2	Q8IEB6	Q8ieb6 plasmodium
37	217	4.6	3452	2	Q8IEA3	Q8iea3 plasmodium
38	215.5	4.6	1524	2	Q8RYN2	Q8ryn2 oryza sativ
39	213.5	4.5	5458	2	Q9U459	Q9u459 plasmodium
40	212.5	4.5	1002	2	Q6CBD5	Q6cbd5 yarrowia li
41	212.5	4.5	5507	2	Q8IHN3	Q8ihn3 plasmodium
42	212	4.5	3471	2	Q6HBX5	Q6hbx5 bacillus th
43	211.5	4.5	3455	2	Q6R5A9	Q6r5a9 tenebrio mo
44	211	4.5	2042	2	Q6BUQ9	Q6buq9 debaryomyce
45	210.5	4.5	1785	2	Q6FS79	Q6fs79 candida gla
46	208.5	4.4	1206	2	Q895S7	Q895s7 clostridium
47	208	4.4	2647	2	Q9U4X0	Q9u4x0 plasmodium
48	207.5	4.4	1409	2	Q7RK24	Q7rk24 plasmodium
49	207	4.4	1417	2	Q871Y7	Q871y7 neurospora
50	206.5	4.4	3472	2	Q632D5	Q632d5 bacillus ce
51	205.5	4.3	3392	2	Q75AD9	Q75ad9 ashbya goss
52	205.5	4.3	3392	2	Q7ZA38	Q7za38 ashbya goss
53	204.5	4.3	1083	2	Q75WB4	Q75wb4 streptococc
54	204	4.3	1790	1	USO1_YEAST	P25386 saccharomyc
55	204	4.3	3404	2	Q7RJB3	Q7rjb3 plasmodium
56	203.5	4.3	1675	2	Q7RHM8	Q7rhm8 plasmodium
57	203	4.3	3504	2	Q8IL45	Q8il45 plasmodium
58	202.5	4.3	2261	2	Q7RJS3	Q7rjs3 plasmodium
59	202.5	4.3	2269	2	Q26223	Q26223 plasmodium
60	201.5	4.3	1078	2	Q963T1	Q963t1 plasmodium
61	201.5	4.3	1873	2	Q9Z4N7	Q9z4n7 enterococcu
62	201.5	4.3	3373	2	Q816D8	Q816d8 bacillus ce
63	201	4.3	1268	2	Q7LGT1	Q7lgt1 saccharomyc
64	201	4.3	1790	2	Q07380	Q07380 saccharomyc
65	201	4.3	2004	2	Q97QP7	Q97qp7 streptococc
66	200.5	4.2	2522	2	Q7RK50	Q7rk50 plasmodium
67	199.5	4.2	1254	2	Q7RGT9	Q7rgt9 plasmodium
68	199.5	4.2	2738	2	Q8IHU4	Q8ihu4 plasmodium
69	198	4.2	1123	2	Q6SZ55	Q6sz55 streptococc
70	198	4.2	1420	2	Q9Y0Y8	Q9y0y8 drosophila
71	197.5	4.2	3692	2	Q8CNU9	Q8cnu9 staphylococ
72	197	4.2	1361	2	Q7REY0	Q7rey0 plasmodium
73	197	4.2	1478	1	BCK1_YEAST	Q01389 saccharomyc
74	197	4.2	2689	2	Q7RES7	Q7res7 plasmodium
75	197	4.2	2720	2	Q6IMC6	Q6imc6 plasmodium
76	197	4.2	18519	2	Q8ISF6	Q8isf6 caenorhabdi
77	197	4.2	18534	2	Q8ISF7	Q8isf7 caenorhabdi
78	196	4.1	1780	2	Q6TV07	Q6tv07 homo sapien
79	196	4.1	1811	2	Q7REH9	Q7reh9 plasmodium
80	195.5	4.1	1139	2	O97237	O97237 plasmodium
81	195.5	4.1	1900	2	Q6VXQ3	Q6vxq3 enterococcu
82	195.5	4.1	1954	2	Q7MIT8	Q7mit8 vibrio vuln
83	195	4.1	1698	2	Q9LC00	Q9lc00 staphylococ
84	195	4.1	2209	2	Q74HA7	Q74ha7 lactobacill
85	195	4.1	2910	2	Q9FND5	Q9fnd5 arabidopsis
86	194.5	4.1	1134	2	Q99051	Q99051 streptococc
87	194.5	4.1	1164	1	BAG_STRAG	P27951 streptococc
88	194	4.1	1126	2	Q8E6U1	Q8e6u1 streptococc
89	193.5	4.1	1125	2	Q98PM9	Q98pm9 mycoplasma
90	193.5	4.1	1524	2	Q7RCM2	Q7rcm2 plasmodium
91	193.5	4.1	3869	2	Q7RN84	Q7rn84 plasmodium
92	193	4.1	1245	2	Q9L470	Q9l470 staphylococ
93	192	4.1	839	2	Q6G315	Q6g315 bartonella
94	192	4.1	1871	2	Q9SRD5	Q9srd5 arabidopsis
95	192	4.1	3009	2	Q7RGG0	Q7rgg0 plasmodium
96	191.5	4.1	1906	2	Q8I3H0	Q8i3h0 plasmodium
97	191	4.0	1534	2	Q9VEH3	Q9veh3 drosophila
98	191	4.0	3111	2	Q9VH10	Q9vh10 drosophila
99	191	4.0	5251	2	Q8IID4	Q8iid4 plasmodium
100	190.5	4.0	1158	2	Q6J5M4	Q6j5m4 streptococc
101	190.5	4.0	2095	2	Q7RN75	Q7rn75 plasmodium
102	190.5	4.0	2276	2	Q79LN3	Q79ln3 staphylococ
103	190.5	4.0	2747	2	Q9BJX9	Q9bjx9 plasmodium
104	190	4.0	1596	2	Q62766	Q62766 rattus norv

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:21 ; Search time 24 Seconds
(without alignments)
3632.183 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MQITYTDDEIQVAKLAGKYT.....IELRLPSGEVIKKNLSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3357	71.0	1039	2	H95115	conserved hypothet
2	3356	71.0	1039	2	D97985	hypothetical prote
3	1307.5	27.7	839	2	G95115	conserved hypothet
4	1245	26.3	853	2	C97985	hypothetical prote
5	946.5	20.0	819	2	B95136	conserved domain p
6	946	20.0	855	2	D98004	histidine Motif-Co
7	636	13.5	802	2	C95136	conserved domain p
8	636	13.5	828	2	E98004	hypothetical prote
9	223.5	4.7	822	2	T46758	hypothetical 92.4K
10	202.5	4.3	2269	2	T28677	rhoptry protein -
11	201.5	4.3	1873	2	T30944	surface protein pr
12	201	4.3	1790	2	S67593	transport protein
13	201	4.3	2004	2	F95133	immunoglobulin A1
14	197	4.2	1478	2	S20117	protein kinase BCK
15	197	4.2	3488	2	T34418	hypothetical prote
16	194.5	4.1	1134	2	A60234	IgA Fc receptor pr
17	194.5	4.1	1164	1	FCSOAG	IgA Fc receptor pr
18	193.5	4.1	1125	2	E90598	membrane nuclease,
19	192	4.1	1871	2	D96796	probable heat shoc
20	190	4.0	4688	2	F82885	hypothetical prote
21	189.5	4.0	2748	2	S57976	nuclear migration
22	189.5	4.0	5005	2	F82884	hypothetical prote
23	189.5	4.0	5327	2	T13564	microtubule-associ
24	186	3.9	1640	2	A24594	probable major sur
25	186	3.9	1658	2	S55101	hypothetical prote
26	185.5	3.9	1983	2	G86643	hypothetical prote
27	185.5	3.9	2109	2	E89066	protein H05009.1 [
28	185.5	3.9	2109	2	T33247	hypothetical prote
29	185	3.9	2485	1	H71621	serine/threonine-s
30	184.5	3.9	1963	2	B98002	IgA-specific metal
31	183	3.9	2218	2	B84683	hypothetical prote
32	182	3.8	2450	2	S71625	protein-tyrosine-p
33	181.5	3.8	1139	1	E64234	cytadherence-acces
34	181	3.8	1939	2	T18372	repeat organellar
35	181	3.8	1979	2	JW0059	mtprd protein - mo
36	181	3.8	2481	2	D90011	FmtB protein [impo
37	180.5	3.8	1185	2	A42404	collagen adhesin -
38	180	3.8	1271	2	A45555	glutamate rich pro
39	180	3.8	1639	2	S05603	major merozoite su
40	179.5	3.8	2447	2	T16870	hypothetical prote
41	179	3.8	1969	2	T38495	hypothetical prote
42	178.5	3.8	763	2	T08929	hypothetical prote
43	177.5	3.8	1881	2	H95076	zinc metalloprotei
44	177	3.7	1305	2	H41662	150K mating aggreg
45	176.5	3.7	2195	2	S61103	SEC16 protein - ye
46	176.5	3.7	2484	2	T26216	hypothetical prote
47	176.5	3.7	2607	2	T26215	hypothetical prote
48	175.5	3.7	1036	2	T30311	S-layer protein -
49	175.5	3.7	1086	2	S16752	major merozoite su
50	175.5	3.7	1231	2	T28681	rib protein - Stre
51	174.5	3.7	1230	2	T22458	hypothetical prote
52	174	3.7	639	2	S20887	actA protein precu
53	174	3.7	1180	2	T20773	hypothetical prote
54	174	3.7	1526	2	A45605	mature-parasite-in
55	174	3.7	3924	2	S37431	ankyrin 2, neurona
56	174	3.7	4549	2	T20771	hypothetical prote
57	173.5	3.7	710	2	S30154	low-temperature-in
58	173.5	3.7	1071	2	E85343	hypothetical prote
59	173	3.7	3147	2	T18674	hypothetical prote
60	172.5	3.6	1032	2	T30270	major tegumental a
61	172	3.6	1631	1	SAZQK1	major merozoite su
62	171.5	3.6	825	2	S26706	transcription fact
63	171	3.6	1240	2	S52734	hypothetical prote
64	171	3.6	2401	2	T28676	rhoptry protein -
65	171	3.6	5170	2	T15348	hypothetical prote
66	170.5	3.6	1545	2	B41859	IgA-specific metal
67	170.5	3.6	1701	2	A54498	major merozoite su
68	170	3.6	1127	2	T25804	hypothetical prote
69	169.5	3.6	857	2	E95009	cell wall surface
70	169	3.6	639	2	AE1100	actin-assembly ind
71	168.5	3.6	1020	2	T29108	hypothetical prote
72	168.5	3.6	1315	2	T28679	fibrinogen-binding
73	168.5	3.6	3135	2	A48584	transmission block
74	168	3.6	1138	2	H86201	hypothetical prote
75	167.5	3.5	1726	1	SAZQGM	major merozoite su
76	166.5	3.5	1233	2	S56271	hypothetical prote
77	166.5	3.5	1612	2	S59969	DNA topoisomerase
78	166.5	3.5	1701	2	A26868	major merozoite su
79	166	3.5	182	2	F97985	hypothetical prote
80	166	3.5	1616	2	G64242	cytadherence-acces
81	165.5	3.5	725	2	T21363	hypothetical prote
82	165	3.5	1650	2	T18444	hypothetical prote
83	165	3.5	1849	2	C41859	IgA-specific metal
84	164.5	3.5	1272	2	C90593	hypothetical prote
85	164.5	3.5	1726	2	A45948	major merozoite su
86	164.5	3.5	1952	2	T48814	hypothetical prote
87	164.5	3.5	3381	2	T42389	versican precursor
88	164	3.5	1948	2	S00485	gene 11-1 protein
89	163.5	3.5	2829	2	A42771	reticulocyte-bindi
90	163	3.4	1385	2	D89824	hypothetical prote
91	163	3.4	1466	2	A36426	SPA2 protein - yea
92	163	3.4	1816	2	F83901	hypothetical prote
93	163	3.4	1837	2	T41023	probable nuclear p
94	163	3.4	2774	2	A43359	microtubule-associ
95	162.5	3.4	766	1	S61694	flocculation suppr
96	162.5	3.4	1368	2	T18371	probable glutamate
97	162.5	3.4	1876	2	E97944	zinc metalloprotei
98	162.5	3.4	2144	2	A97942	metalloproteinase
99	162.5	3.4	26926	1	I38344	titin, cardiac mus
100	162	3.4	1161	2	C97881	conserved hypothet
101	161.5	3.4	1080	2	T43164	IactA protein - Li
102	161.5	3.4	1252	2	B42771	reticulocyte-bindi